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(p27 [Kip1])

1 ATGTCAAACGTGCGAGTGTCTAACGGGAGCCCTAGCCTGGAGCGG
MetSerAsnValArgValSerAsnGlySerProSerLeuGluArg

46 ATGGACGCCAGGCAGGCGGAGCACCCCAAGCCCTCGGCCTGCAGG
MetAspAlaArgGlnAlaGluHisProLysProSerAlaCysArg

91 AACCTCTTCGGCCCCGGTGGACCACGAAGAGTTAACCCGGGACTTG
AsnLeuPheGlyProValAspHisGluGluLeuThrArgAspLeu

136 GAGAAGCACTGCAGAGACATGGAAGAGGCGAGCCAGCGCAAGTGG
GluLysHisCysArgAspMetGluGluAlaSerGlnArgLysTrp

181 AATTTTCGATTTTCAGAATCACAAACCCCTAGAGGGCAAGTACGAG
AsnPheAspPheGlnAsnHisLysProLeuGluGlyLysTyrGlu

226 TGGCAAGAGGTGGAGAAGGGCAGCTTGCCCGAGTTCTACTACAGA
TrpGlnGluValGluLysGlySerLeuProGluPheTyrTyrArg

271 CCCCCGCGCCCCCAAGGTGCCTGCAAGGTGCCGGCGCAGGAG
ProProArgProProLysGlyAlaCysLysValProAlaGlnGlu

316 AGCCAGGATGTCAGCGGGAGCCGCCCCGGCGGCCCTTTAATTGGG
SerGlnAspValSerGlySerArgProAlaAlaProLeuIleGly

361 GCTCCGGCTAACTCTGAGGACACGCATTTGGTGGACCCAAAGACT
AlaProAlaAsnSerGluAspThrHisLeuValAspProLysThr

406 GATCCGTCGGACAGCCAGACGGGGTTAGCGGAGCAATGCGCAGGA
AspProSerAspSerGlnThrGlyLeuAlaGluGlnCysAlaGly

451 ATAAGGAAGCGACCTGCAACCGACGATTCTTCTACTCAAAACAAA
IleArgLysArgProAlaThrAspAspSerSerThrGlnAsnLys

496 AGAGCCAACAGAACAGAAGAAAATGTTTCAGACGGTTCCCCAAAT
ArgAlaAsnArgThrGluGluAsnValSerAspGlySerProAsn

541 GCCGGTTCTGTGGAGCAGACGCCCAAGAAGCCTGGCCTCAGAAGA
AlaGlySerValGluGlnThrProLysLysProGlyLeuArgArg

586 CGTCAAACGTAA
ArgGlnThr

Fig. 1

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FKBP-12 SEQUENCE

1 GCCGCCGCCATGGGAGTGCAGGTGGAAACCATCTCCCCAGGAGAC
 MetGlyValGlnValGluThrIleSerProGlyAsp

46 GGGCGCACCTTCCCCAAGCGCGGCCAGACCTGCGTGGTGCACCTAC
 GlyArgThrPheProLysArgGlyGlnThrCysValValHisTyr

91 ACCGGGATGCTTGAAGATGGAAAGAAATTTGATTCTCCCGGGAC
 ThrGlyMetLeuGluAspGlyLysLysPheAspSerSerArgAsp

136 AGAAACAAGCCCTTTAAGTTTATGCTAGGCAAGCAGGAGGTGATC
 ArgAsnLysProPheLysPheMetLeuGlyLysGlnGluValIle

181 CGAGGCTGGGAAGAAGGGGTTGCCCAGATGAGTGTGGGTCAGAGA
 ArgGlyTrpGluGluGlyValAlaGlnMetSerValGlyGlnArg

226 GCCAAACTGACTATATCTCCAGATTATGCCTATGGTGCCACTGGG
 AlaLysLeuThrIleSerProAspTyrAlaTyrGlyAlaThrGly

271 CACCCAGGCATCATCCCACCACATGCCACTCTCGTCTTCGATGTG
 HisProGlyIleIleProProHisAlaThrLeuValPheAspVal

316 GAGCTTCTAAAACCTGGAATGACAGGAATGGCCTCCTCCCTTAGCT
 GluLeuLeuLysLeuGlu

361 CCCTGTTCTTGGATCTGCCTGGAGGGATCTGGTGCCTCCAGACAT
406 GTGCACATGATCCATATGGAGCTTTTCCTGATGTTCCACTCCACT
451 TTGTATAGACATCTGCCCTGACTGAATGTGTTCTGTCACTCAGCT
496 TTGCTTCCGACACCTCTGTTTCCTCTTCCCCTTTCTCCTCGTATG
541 TGTGTTTACCTAAACTATATGCCATAAACCTCAAGTTATTCA

Fig. 2

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DEMONSTRATION OF THE
P27(KIP1):FKBP12 INTERACTION

	P27(Kip1)	A1	B1
CDK2	+	-	-
FKBP-12	+	-	-
TRK	-	-	-
CYC-B	-	-	-
Vector	-	-	-

Fig. 3